

## FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331  
<subunit 1 of 1, 1184 aa, 1 stop  
<MW: 129022, pI: 5.20, NX(S/T): 5  
MMQLLQLLLGLLPGGYLFLLGDCQEVTTTLTVKYQVSEEVPSGTVIGKLSQELGREBERRQA  
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLLDREQLCRQWDCLVSDVLATGDLALIHVEIQ  
VLDINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNLTHTYTLSPSEHFALDQVIV  
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNDNSPAPAESS  
LALIEQEDAAPGTLTIKLATDPDQGPNGEVEFFLSKHMPEVLDTFSIDAKTGQVILRRPL  
DYEKNPAYEVDVQARDLGNPIPAHCKVLIKVLVDNDNIPSIHVTWASQPSLVSEALPKDSF  
IALVMADDLDLSDGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLAQD  
QQLQPLSAKKQLLSIQISDINDNAPVFEKSRYEVSSTRENNLPSLHLITIKAHDADLNGKVS  
YRIQDSPVAHLVAIDSVTGEVTAQRSLNVEEMAGFEFQVIAEDSGQPLASSVSVVWSLLDA  
NDNAPEVVQFVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTTPPLATHSSRPFLTT  
IVARDADSGANGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS  
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK  
KDNRAYNCREAESTYRQPKRPQKHQKADIHLVPLRGQAGEPCEVGQSHKDVDKEAMMEA  
GWDPCIQAPFHLTPTLYRTLNRQNGGAPAESREVLQDTVNLLFNHPRQRNASRENLNLP  
QPATGQPRSRPLKVAGSPTGRLAGDQGSEAPQRPASSATLRRQRHLNGKVSPEKESGPRQ  
ILRSLVRLSVAAFAERNPVEELTVDSPPVQQISQLLSLLHQGFQPKPNHRGNKYLAKEGGS  
RSAIPDTDGFSARAGGQTDPEQEEGFLDPEEDLSVKQLLEELSSLLDPSTGLALDRLSAPD  
PAWMARLSLPLTTNRYRDNVISPDAAATEEPRTFTQTFGKAEAPELSPTGTRLASTFVSEMSL  
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSLDLATSAAAGMKVQGDPGGKTGTEGKSRGSS  
SSSRCL

### **Important features:**

#### **Signal peptide:**

amino acids 1-13

#### **Transmembrane domain:**

amino acids 719-739

#### **N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

#### **Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

0972295-10534

## FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGG  
CAGACCGTGTGAGGGGGCCTGTGGCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG  
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCTCATCGACTCCAGCATCATGATTACCT  
CCCAGATACTATTTTTTGGATTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT  
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGCAACCAT  
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCAC  
GGAAATGAACCTGTGTGTAATCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTCATTGGC  
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AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGACTCTC  
ATGGCTCTTCTTCTGAGTTTGGTGCTGTCAACTGCCCATACACTTACATGCTTACTTCTCT  
CAGGAATGTGACTGACACGGATATTCTGACCTTGAACGGCGACTGCTGCAAAACCATGGATA  
TGATCATAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAAATGTTCCAGAAGGGGGAA  
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTACCACCTCAGCATCAGG  
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC  
TTTTTCTGGAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC  
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CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCCAAAGAGGCA  
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTGTGCCAACACATT  
TCCTTCAATCTTGTGGAATAATCATCGTCACATCCATCAGAGGATGCTGATCACTCTTAC  
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTCCCAATGTCTTGTCTGCTATTAGCAC  
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCCTTAGAA  
TACCGCACCATAACTCACTGAAGTCTTGGAGAACTGCAGTTCAACTTCTATCACCGGTTGGTT  
TGATGTGATCTTCTGGTCAGCGCTCTCTTAGCATACTTCTCTCTATTTGGCTCACAAAC  
AGGCACCAGAGAAGCAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT  
GGTTTCAAATTTAGATATAAGAGGGGGGAAAAATGGAACGAGGCGCTGACATTTTATAAAC  
AAACAAAATGCTATGGTAGCATTTTTACCTTCATAGCATACTCCTTCCCGCTCAGGTGATA  
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA  
GCAGAGAGCATCCGCTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGCCAAGAACTAA  
AGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACAGT  
AGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT  
AAAATCAGAGACTGTAACAAAAAAGGGGCGCGCGACTCTAGAGTCG  
ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTATTATTCAGCTTATAATG

097825.17170

## FIGURE 173

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI  
LGVLNSSSRYPFHWMNLCVILLILVFMVPPYIGYFIVSNIRLLHKQRLLFSCLLWLTFFMYFF  
WKLGDPPFIPILSPKHGILSIEQLISRVGIVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDDI  
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFGWMIKSVTTSASGSENLTLIQ  
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF  
DRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISS  
SKSSNVIVLLLAQIMGMYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA  
LSSILFLYLAHKQAPEKQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

#### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

#### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160

0973295.101501  
105101.5028760